

Amendments to the Claims

This listing of claims replaces all prior versions, and listings, of claims in the above-identified application:

1-46. **(Canceled)**

47. **(Currently Amended)** A method for crystallizing ~~[[an]]~~ *S. aureus* thioredoxin reductase ~~molecule or molecular complex~~ comprising:

preparing purified *S. aureus* thioredoxin reductase at a concentration of about 1 mg/ml to about 50 mg/ml, wherein the amino acid sequence of the *S. aureus* thioredoxin reductase comprises SEQ ID NO:1, or SEQ ID NO:1, except that at least one methionine is replaced with selenomethionine; and

crystallizing *S. aureus* thioredoxin reductase from a solution at a pH of about 6 to about 10 and comprising about 0 wt. % to about 40 wt. % DMSO and about 100 mM to about 6 M sodium formate.

48. **(Original)** A crystal of *S. aureus* thioredoxin reductase.

49. **(Original)** The crystal of claim 48 having the tetragonal space group symmetry $P4_32_12$.

50. **(Original)** The crystal of claim 48 comprising a unit cell having dimensions a, b, and c; wherein a is about 70Å to about 110Å, b is about 70Å to about 110Å, c is about 160Å to about 220Å, and $\alpha = \beta = \gamma = 90^\circ$.

51. **(Original)** The crystal of claim 48 comprising atoms arranged in a spatial relationship represented by the structure coordinates listed in Table 1.

52. (Currently Amended) ~~A~~ The crystal of ~~claim 48~~ *S. aureus* thioredoxin reductase, wherein the thioredoxin reductase has amino acid sequence SEQ ID NO:1.

53. (Currently Amended) ~~A~~ The crystal of ~~claim 48~~ *S. aureus* thioredoxin reductase, wherein the thioredoxin reductase has amino acid sequence SEQ ID NO:1, except that at least one methionine is replaced with selenomethionine.

54. (New) A crystal of *S. aureus* thioredoxin reductase having tetragonal space group symmetry $P4_32_12$ and comprising a unit cell having dimensions a, b, and c; wherein a is about 70Å to about 110Å, b is about 70Å to about 110Å, c is about 160Å to about 220Å, and $\alpha = \beta = \gamma = 90^\circ$.

55. (New) A polypeptide consisting of a portion of *S. aureus* thioredoxin reductase starting at one of amino acids 10 to 12 and ending at one of amino acids 290 to 297 of *S. aureus* thioredoxin reductase as set forth in SEQ ID NO:1.

56. (New) The polypeptide of claim 55, wherein the three-dimensional configuration of the amino acids listed in Table 2, is defined by a set of points having a root mean square deviation of less than about 1.1 Å from points representing the backbone atoms of said amino acids as represented by structure coordinates listed in Table 1.

57. (New) The polypeptide of claim 55, wherein the three-dimensional configuration of the amino acids listed in Table 3, is defined by a set of points having a root mean square deviation of less than about 1.1 Å from points representing the backbone atoms of said amino acids as represented by structure coordinates listed in Table 1.

58. (New) The polypeptide of claim 55, wherein the three-dimensional configuration of the amino acids listed in Table 4, is defined by a set of points having a root mean square deviation of less than about 1.1 Å from points representing the backbone atoms of said amino acids as represented by structure coordinates listed in Table 1.

59. (New) A polypeptide consisting of a portion of *S. aureus* thioredoxin reductase starting at one of amino acids 43 to 52 and ending at one of amino acids 286 to 289 of *S. aureus* thioredoxin reductase as set forth in SEQ ID NO:1.

60. (New) The polypeptide of claim 59, wherein the three-dimensional configuration of Cys 135, Cys 138, and the amino acids listed in Table 5, is defined by a set of points having a root mean square deviation of less than about 0.8 Å from points representing the backbone atoms of said amino acids as represented by structure coordinates listed in Table 1.

61. (New) The polypeptide of claim 59, wherein the three-dimensional configuration of Cys 135, Cys 138, and the amino acids listed in Table 6, is defined by a set of points having a root mean square deviation of less than about 0.8 Å from points representing the backbone atoms of said amino acids as represented by structure coordinates listed in Table 1.

62. (New) The polypeptide of claim 59, wherein the three-dimensional configuration of Cys 135, Cys 138, and the amino acids listed in Table 7, is defined by a set of points having a root mean square deviation of less than about 0.8 Å from points representing the backbone atoms of said amino acids as represented by structure coordinates listed in Table 1.